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The present sequence represents a monocyte nature differentiation factor (MNDP) which maintains the life of macrophages for long periods in liquid culture. MNDP can be used as an anti-cancer agent, an immune activator and to treat infectious diseases.

The present sequence represents a monocyte-macrophage differentiation factor (MDMF) which maintains the life of macrophages for long periods in liquid culture. MDMF can be used as an anti-cancer agent, an immune activator and to treat infectious diseases.

PT useful in diagnosis and treatment of vascular disease caused by  
arteriosclerosis -  
PS  
XX  
Claim 60, Page 345-346; 679PP; Japanese.  
The present invention provides the protein and coding sequences of a .





QY	241	KTCGNGISTRVNDNPCLRMEKTCRCEVPGQPGVLSKKGCKSKCKSKTPPEVRY	300
Db	315		374
Db	315	KTCGNGISTRVNDNPCLRMEKTCRCEVPGQPGVLSKKGCKSKCKSKTPPEVRY	374
QY	301	ACCLSVKYKPYCSCYDRCFCFLTQVTRVRREREDDEDEFSKNNMQLQSCCKNYP	360
Db	375		434
QY	361	HANEAAFPYRFLNDIKFED	381
Db	435	HANEAAFPYRFLNDIKFED	455
RESULT 7			
ID	AAW35730	standard; protein: 381 AA.	
AC	AAW35730;		
DT	27-MAR-1998	(first entry)	
XX			
DE	Human cysteine rich protein 61 (Cyr61).		
XX			
KN	Cysteine rich Protein 61; Cyr61; human;		
KN	extracellular matrix signalling molecule; cell adhesion;		
KN	cell migration; cell proliferation; angiogenesis; chondrogenesis;		
XX	oncogenesis; haemostasis; wound healing; organ regeneration;		
OS	Home sapiens.		
XX			
PN	W0973395-A2.		
XX			
PD	18-SEP-1997.		
XX			
PF	14-MAR-1997;	97W0-WS04193.	
XX			
PR	15-MAR-1996;	96US-0013958.	
XX			
PA	(MUNI) - MUNIN CORP.		
XX			
PT	Lau LF;		
XX			
DR	WPI. 1997-470075/43.		
DR	N-PSDB; AAH94699.		
XX			
XX			
PT	Isolated and purified cysteine rich protein 61, Cyr61 - useful to modulate e.g. haemostasis, induce wound healing, promote organ regeneration etc		
PT	Regeneration etc		
XX			
FS	Claim 2: Page 112-113, 13PP; English.		
XX			
CC	This protein sequence comprises human cysteine rich protein 61 (Cyr61), an extracellular matrix signalling molecule. Its amino acid sequence was deduced from a human placental cDNA clone (see AAI14391). Human proteins can be expressed in transformed or transfected host cells. Cyr61 can be used to modulate oxygen homeostasis, i.e. gene wound healing in a tissue, promote angiogenesis, (chimeric) tissue grafting, promote organogenesis, modulator of angiogenesis, chondrogenesis, oncogenesis, cell adhesion, cell migration, cell proliferation, cell differentiation, endow a population of undifferentiated hematopoietic stem cells in culture and to screen for a miton (claimed). Ex vivo methods for using the mammalian extracellular matrix signalling molecules to prepare blood products are also provided.		
CC			
CC	Sequence 381 AA;		
SO			
Query Match	99.6%	Score 2106; DB 18;	Length 381;
Best Local Similarity	99.5%	Def. No. 2.5e-153;	
Matches	379;	1; Mismatches 1;	Indels 0;
		Gaps 0;	



OS	Unidentified.	AC	AAR0919;
XX		XX	
PN	US20020430411.	DT	25-JUN-1996 (first entry)
XX		XX	
PD	25-APR-2002.	DE	connective tissue growth factor-2.
XX		XX	
PF	14-MAY-2001; 2001US-0859625.	KW	crgf-2, connective tissue growth factor-2; secreted protein;
XX		KW	cartilagenous growth; skeletal; embryo; cell growth; morphogenesis;
PR	06-JUN-1995; 95US-046847.	KW	insulin-like growth factor; fibroblast growth factor; cryo1.
PR	01-APR-1998; 98US-0055587.	XX	
XX		OS	
PT	(HAST/ HASTINGS G. A.	XX	
PA		PT	
PA	(ADAM) ADAMS M. D.	PT	
XX		PD	
PT	Hastings GA, Adams MD;	PD	
XX		XX	
DR	WPI: 2002-362150/41.	XX	
XX		XX	
PT	Novel isolated polynucleotide sequence encoding a human small CCN-like	XX	
PT	growth factor, useful for treating muscle wasting disease, and	XX	
PT	osteoporosis.	XX	
XX		OS	
PB	Disclosure: Fig 2A-D: 37pp; English.	XX	
XX		XX	
CC	The present invention describes human small CCN-like growth factor	XX	
CC	(SCGF). SCGF has voluntary and osteopathic activities, and can be used	XX	
CC	in gene therapy. The SCGF polypeptides and polynucleotides can be used	XX	
CC	for treating muscle wasting diseases, and osteoporosis, and to stimulate	XX	
CC	wound healing and tissue regeneration, to promote angiogenesis and to	XX	
CC	stimulate proliferation of vascular smooth muscle and endothelial cell	XX	
CC	production. The present sequence represents a CCN family protein which	XX	
CC	is given in comparison with the human SCGF in the exemplification of the	XX	
CC	present invention.	XX	
SQ	Sequence 374 AA:	XX	
Query Match	93.6%; Score 1980.5; DB 23; Length 374;	XX	
Best Local Similarity	96.3%; Pred. No. 1e-143;	XX	
Matches	360; Conservative 1; Mismatches 12; Indels 1; Gaps 1;	XX	
OY	1 MSSRARAALVWVLUHTRIALUSTPACPCPACPKAAGPGVQWDRDCCCKVAKOL 60	CC	connective tissue growth factor-2 (crgf-2) is encoded by a cDNA
DB	1 MSSRTVRELALVWVLUHTRVGLSTPACPCPACPKAAGPGVQWDRDCCCKVAKOL 60	CC	(AAT285) isolated from a human fetal lung cDNA library. The SCGF
OY	61 NECCRTKTOPDHKGKLENGEAGSASTALGKTCRQAQSGRCEPCYNSRYKONGESTPCKHQ 120	CC	polypeptides are structurally and functionally related to a family
DB	61 NECCRTKTOPDHKGKLENGEAGSASTALGKTCRQAQSGRCEPCYNSRYKONGESTPCKHQ 120	CC	of growth factors which include TGF (insulin-like growth factor),
OY	62 NECCRTKTOPDHKGKLENGEAGSASTALGKTCRQAQSGRCEPCYNSRYKONGESTPCKHQ 120	CC	PIGF (platelet-derived growth factor), and FGF (fibroblast growth
DB	62 NECCRTKTOPDHKGKLENGEAGSASTALGKTCRQAQSGRCEPCYNSRYKONGESTPCKHQ 120	CC	factor). crgf-2 exhibits 89 percent identity and 93 percent similarity
OY	121 CTCGDAAG-CIPCQELSPSLNPCCGPKRQVYTCQCEWWDSDSKPMDGQGIL 179	CC	to croyl. Croyl is a growth factor-inducible immediate early gene
DB	121 CTCGDAAG-CIPCQELSPSLNPCCGPKRQVYTCQCEWWDSDSKPMDGQGIL 179	CC	initially identified in serum-stimulated mouse fibroblasts. It encodes
OY	121 CTCGDAAG-CIPCQELSPSLNPCCGPKRQVYTCQCEWWDSDSKPMDGQGIL 180	CC	a member of an emerging family of secreted proteins which are also a
DB	180 GKELEDFSEVETRNNEILAVKGSSKRRPKPFGQEPRYMLPQGOKCIVOTPSOC 239	CC	group of cysteine-rich proteins. This group of GPs are important for
OY	180 GKELEDFSEVETRNNEILAVKGSSKRRPKPFGQEPRYMLPQGOKCIVOTPSOC 239	CC	normal growth, differentiation, morphogenesis of the cartilaginous
DB	181 GKELEDFSEVETRNNEILAVKGSSKRRPKPFGQEPRYMLPQGOKCIVOTPSOC 240	CC	skeleton of an embryo and cell growth.
SQ	Sequence 375 AA:	XX	
Query Match	93.6%; Score 1980.5; DB 17; Length 375;	XX	
Best Local Similarity	96.3%; Pred. No. 1e-143;	XX	
Matches	360; Conservative 1; Mismatches 12; Indels 1; Gaps 1;	XX	
OY	1 MSSRARAALVWVLUHTRIALUSTPACPCPACPKAAGPGVQWDRDCCCKVAKOL 60	CC	
DB	1 MSSRTVRELALVWVLUHTRVGLSTPACPCPACPKAAGPGVQWDRDCCCKVAKOL 60	CC	
OY	300 YACCSVKEVKPKCYSQDCCCTQPLTRVKNRREDEDETEKNSVMMQSKNCYNC 359	CC	
DB	301 YACCSVKEVKPKCYSQDCCCTQPLTRVKNRREDEDETEKNSVMMQSKNCYNC 360	CC	
OY	360 PHANRARPYRFL 373	CC	
DB	361 PHANRARPYRFL 374	CC	
RESULT 10		XX	
ARR0919		XX	
ID	AAR0919 standard; Protein: 375 AA.	XX	

QY 240 SKTCGCTISTRVTDNEPCELUKETRICEVRCGCPYVSSILKKGKSKTKSKPSPPVIFT 299  
 Db 241 SKTCGCTISTRVTDNEPCELUKETRICEVRCGCPYVSSILKKGKSKTKSKPSPPVIFT 300  
 QY 300 VAGCISKSYKTRKRYCGCGVCGRCCPOLTYKMPKFRCEGETESPKVNMIMIQCXNC 359  
 Db 301 VAGCISKSYKTRKRYCGCGVCGRCCPOLTYKMPKFRCEGETESPKVNMIMIQCXNC 360  
 QY 360 PHANEAFFPYPYLF 373  
 Db 361 PHANEAFFPYPYLF 374

RESULT 11

AAV31620  
 ID AAV31620 standard; Protein: 375 AA.  
 XX  
 AC AAV31620:  
 XX  
 DR 02-NOV-1999 (first entry)  
 XX  
 DE Human CTGF-2.  
 XX  
 KW Connective tissue growth factor-2; wound healing; bone disorder;  
 KW skin disorder; acne; burn; UV damage; stabilisation; tissue implant.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Peptide  
 FT 1..24  
 FT /label= signal\_peptide  
 FT 25..375  
 FT Protein  
 FT Mac-difference 268  
 FT /note= \*Cys encoded by IGT\*  
 PN US5945300-A.  
 XX  
 PD 31-AUG-1999.  
 XX  
 PP 02-JUN-1995; 95US-0459101.  
 XX  
 PR 02-JUN-1995; 95US-0459101.  
 XX  
 PR 12-JUL-1994; 94WO-US07736.  
 PA (ADAM) ADAMS M D.  
 PA (LTHH) LI H.  
 XX  
 PT Adams MD, LI H;  
 XX  
 DR WPI; AAV31720.  
 N-PSDB: AAV31720.

This sequence represents human connective tissue growth factor-2 (CTGF-2). CTGF-2 cDNA was isolated from a cDNA library derived from human foetal lung. In one instance, the cDNA was cloned into a baculovirus expression vector, having first been amplified and modified via PCR using primers AAZ1121 and AAZ1122. In another instance, the cDNA was cloned into a COS cell expression vector with prior amplification and modification using PCR primers AAZ1173 and AAZ1174. CTGF-2 is structurally and functionally related to family of growth factors which include IGF (insulin-like growth factor), PDGF (platelet-derived growth factor), and RGF (fibroblast growth factor). This emerging family of cysteine-rich secreted proteins are important for normal growth differentiation pathways of the extracellular matrix. The skeleton, embryo, and cell growth functions also include wound healing, tissue repair, implant fixation and stimulating increased bone mass. CTGF-2 may be used to enhance the repair of connective tissue and

CC support tissue and can therefore treat skin disorders e.g., acne, aging, UV damage or burns. CTGF-2 can be used to promote the attachment, fixation and stabilisation of tissue implants inserted during reconstructive surgery and can be used to enhance the healing of external wounds. It can be used in the treatment of injured or depleted bone as it promotes the growth of connective tissue, bone and cartilage and stimulates protein and collagen synthesis.

XX

Sequence 375 AA;

QY Every Match 93 64; Score 1980 5; DB 20; Length 375;  
 Best Local Similarity 96 38; Pred No 1a-1a3; 1; Mismatches 12; Indels 1; Gaps 1;  
 Matches 360; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MSRTIAALAVVYUHILHMLAISCTPAACTHPCPAPKCPAPVGLVRSOGCGCKVCKQL 60  
 Db 1 MSRTIAALAVVYUHILHMLAISCTPAACTHPCPAPKCPAPVGLVRSOGCGCKVCKQL 60  
 QY 61 NEPDSSKPOCPDKTCKLNGASSPAKLGICHAESPRPEENSYVQESPKHQ 120  
 Db 61 NEPDSSKPOCPDKTCKLNGASSPAKLGICHAESPRPEENSYVQESPKHQ 120  
 QY 121 CTCGDAVG-CIPCPDLSITGCPNPLVKGCGCWEWCEISKDPHEKQ 179  
 Db 121 CTCGDAVG-CIPCPDLSITGCPNPLVKGCGCWEWCEISKDPHEKQ 179  
 QY 180 GHEGFDASPEVLRNNEELANGKSSKLLKVKMPRPLNPQKIVOTSSQ 239  
 Db 181 GHEGFDASPEVLRNNEELANGKSSKLLKVKMPRPLNPQKIVOTSSQ 239  
 QY 240 SKTCGCTISTRVTDNEPCELUKETRICEVRCGCPYVSSILKKGKSKTKSKPSPPVIFT 299  
 Db 241 SKTCGCTISTRVTDNEPCELUKETRICEVRCGCPYVSSILKKGKSKTKSKPSPPVIFT 300  
 QY 300 VAGCISKSYKTRKRYCGCGVCGRCCPOLTYKMPKFRCEGETESPKVNMIMIQCXNC 359  
 Db 301 VAGCISKSYKTRKRYCGCGVCGRCCPOLTYKMPKFRCEGETESPKVNMIMIQCXNC 360  
 QY 360 PHANEAFFPYPYLF 373  
 Db 361 PHANEAFFPYPYLF 374

RESULT 12

AAE18108  
 ID AAE18108 standard; Protein: 375 AA.  
 XX  
 AC AAE18108;  
 XX  
 DT 07-MAY-2002 (first entry)  
 XX  
 DE Human alternative connective tissue growth factor-2 (CTGF-2).  
 XX  
 KW Human; angiogenesis; connective tissue growth factor-2; CTGF-2; tumour; ischaemic; restenosis; tissue repair; wound healing; congenital defect; cardiovascular disease; atherosclerosis; heart failure; arrhythmia; bursitis; osteoporosis; Periodontal disease; liver failure; tracheal; vascular; cosmetic; plastic surgery; vasotropic; hepatotropic; ulcer; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200204480-12.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PR 11-JUL-2001; 2001WO-US21799.  
 PR 11-JUL-2000; 2000US-217407P.  
 PR 18-MAY-2001; 2001US-291647P.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 PR (TNGE-) TRANSGENE SA.

XX	PT	Li, H., Adams MD, Calenda V, Pataccioi V;	DT	18-JAN-1993 (first entry)
XX	DR	WPI: 2002-171998/22.	DD	Beta-1G-M1.
XX	DR	N/PSDB, RADD999.	XX	Transforming growth factor beta, induced: CEF-10; v-src: chicken; embryo; fibroblasts; TGF-beta.
XX	PT	Stimulating angiogenesis in a mammal, preferably human, having ischemia or necrosis, or is treated for limb revascularization, by administering connective tissue growth factor 2 polypeptide or polynucleotide.	XX	Mus musculus.
PS	PS	Disclosure: FIG 11, 131pp; English.	XX	
XX	CC	The present invention relates to a method for stimulating angiogenesis in a mammal, the method comprises administering a polynucleotide encoding connective tissue growth factor-2 (CTGF-2) or an active fragment or its derivative. The method is useful for stimulating angiogenesis in a mammal, preferably human, having ischemia or necrosis, or is treated for limb revascularization which is 1/16th of a leg or arm. The invention is useful for initiating, enhancing, promoting, repairing, and stabilizing connective tissue, repairing connective tissue, repairing connective tissue, promoting the attachment, fixation and stabilization of tissue implants and enhancing wound healing, hence, is useful for treating cardiovascular disease, e.g., myocardial infarcts, and is also useful to differentiate, proliferate and attract cells leading to regeneration of tissues which is utilized to repair, replace or protect tissue damaged by congenital defects, trauma, burns, ulcer, etc., e.g., disease (e.g., osteoporosis, periodontal disease, liver failure), surgery including cosmetic, plastic surgery. The present sequence is human alternative CTGF-2. CTGF-2 gene is useful in gene therapy.	XX	
XX	SO	Sequence 375 AA:	XX	
Query Match	93.6%	Score 1980.5; DB 23; Length 375;	PR	18-JAN-1991 91US-064991.
Best Local Similarity	96.3%	Pred. No. 1-143; 12; Indels 1; Gaps 1;	PR	10-JAN-1992 9408-0016270.
Matches	360;	Conservative 1; Mismatches 12; Indels 1; Gaps 1;	PA	(BRM) BRISTOL-MERYS SOUTHERN CO.
OY	1	MSSRALARLAVVLTUHLTRALSTPAPCPIPLPKCARGVGLVQDCCVKVAKL 60	PI	Brunner AM, Chinn J, Neubauer MG, Purchio AF;
OY	1	MSSRVRVRLAVVLTUHLTRALSTPAPCPIPLPKCARGVGLVQDCCVKVAKL 60	XX	WPI: 1992-2435093.
DB	61	NECCKSTOPCHKGKGEGNGEASSTALKIGCRAQSBRGRCREYNSRYVONGSSTOPCKHQ 120	DR	N/PSDB, RAQ6621.
OY	61	NECCKSTOPCHKGKGEGNGEASSTALKIGCRAQSBRGRCREYNSRYVONGSSTOPCKHQ 120	XX	
DB	61	NECCKSTOPCHKGKGEGNGEASSTALKIGCRAQSBRGRCREYNSRYVONGSSTOPCKHQ 120	XX	
OY	121	CTGDAVAGCIPCPOLSLPQGCPAPRIVVYQGCCWQDSKIPMDGGL 179	XX	
DB	121	CTGDAVAGCIPCPOLSLPQGCPAPRIVVYQGCCWQDSKIPMDGGL 179	XX	
OY	180	GKELFDSAEVEVTRNNELAVKGSSSKRUPFGPRIMPLAGONCIVWPTWSOC 239	XX	
DB	181	GKELFDSAEVEVTRNNELAVKGSSSKRUPFGPRIMPLAGONCIVWPTWSOC 240	XX	
OY	240	SKTCGIGSTVNDNPICRVLVETICEVPGCQVWSSKKCKCSKTKSKP 299	SO	Sequence 379 AA:
DB	241	SKTCGIGSTVNDNPICRVLVETICEVPGCQVWSSKKCKCSKTKSKP 300	Query Match	91.6%; Score 1938; DB 13; Length 379;
OY	300	YACCSVVKRPPYCPGCGDRCCTPQTRVVKMRPDEGETTSKVNMMQSKNC 359	Best Local Similarity	91.4%; Pred. No. 1-5e-140; 9; Mismatches 18; Indels 6; Gaps 2;
DB	301	YACCSVVKRPPYCPGCGDRCCTPQTRVVKMRPDEGETTSKVNMMQSKNC 360	CC	1 MSSRALARLAVVLTUHLTRALSTPAPCPIPLPKCARGVGLVQDCCVKVAKL 60
OY	360	PHANAAFPYRFL 373	DB	1 MSSRVRVRLAVVLTUHLTRALSTPAPCPIPLPKCARGVGLVQDCCVKVAKL 60
DB	361	PHANAAFPYRFL 374	QY	61 NECCKSTOPCHKGKGEGNGEASSTALKIGCRAQSBRGRCREYNSRYVONGSSTOPCKHQ 120
RESULT 13	ID	AAK1555 standard; Protein: 379 AA.	DB	61 NECCKSTOPCHKGKGEGNGEASSTALKIGCRAQSBRGRCREYNSRYVONGSSTOPCKHQ 120
AAK1555	XX		121 CTGDAVAGCIPCPOLSLPQGCPAPRIVVYQGCCWQDSKIPMDGGL 179	
AC	AAK1555;		121 CTGDAVAGCIPCPOLSLPQGCPAPRIVVYQGCCWQDSKIPMDGGL 178	
XX			181 GELFDSAEVEVTRNNELAVKGSSSKRUPFGPRIMPLAGONCIVWPTWSOC 238	



XX  
DR  
XX  
PT  
PT  
PT  
PT  
XX  
XX

WPI: 2002-382150/41.

Novel isolated polynucleotide sequence encoding a human small CCN-like growth factor, useful for treating muscle wasting disease, and osteoporosis.

Disclosure: FIG 2A-D; 31pp; English.

The present invention describes human small CCN-like growth factor (ScGF). ScGF has mitogenic and osteogenic activities, and can be used in gene therapy. The ScGF Polypeptides and polynucleotides can be used for treating muscle wasting diseases, and osteoporosis, and to stimulate wound healing and tissue regeneration, to promote angiogenesis, and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CCN family protein which is given in comparison with the human ScGF in the exemplification of the present invention.

Sequence 379 AA.

Query Match, Best Locality, similarity, Score, DB, Length.

Best Locality: 91.6%; Score: 1939; DB: 23; Length: 379;

Matches 350; Prey: No. 1.8e-140; Pred: No. 1.8e-140; Mismatches: 9; Indels: 6; Gaps: 2;

QY 1 MESSRARRALAVVTTLHTRALALSCPAPRCKPAPKAPGPGVLRGCGCCVKVANQL 60  
DB 1 MSSSPFRILAVAVTLLHTRALALSCPAPRCKPAPKAPGPGVLRGCGCCVKVANQL 60

QY 61 NEDCCKTQEPDHTRKSLIGNGASSPAALKGICRQASSEGRPEYNSRYYONGSQPACHQ 120  
DB 61 NEDCCKTQEPDHTRKSLIGNGASSPAALKGICRQASSEGRPEYNSRYYONGSQPACHQ 120

QY 121 CTCINGANGCIPCPQOELSLPUNPGSPNPRLUVKYTCRQSGCCEBWWEDDSKDMEDQDG 180  
DB 121 CTCINGANGCIPCPQOELSLPUNPGSPNPRLUVKYTCRQSGCCEBWWEDDSKDSLDDDD-- 178

QY 181 KELGDASSEVLTTRNNELIAGKGSSLRKPVHGSPRLYNEI--QSQKQTVQTMHSQ 239  
DB 179 -LIGDASSEVLTTRNNELIAGKGSSLRKPVHGSPRLYNEI--QSQKQTVQTMHSQ 236

QY 239 CSKTGEGIISRTNDNEPRLVKETRACEYRUCGQPVYSSLRKGKSKTKASPPRF 298  
DB 237 CSKTGEGIISRTNDNEPRLVKETRACEYRUCGQPVYSSLRKGKSKTKASPPRF 296

QY 299 TTAGLSKSYKRYKCGCGDGCCTPDLTRKRFKEDGCTTSKWMHIOSKCWN 358  
DB 297 TTAGLSKSYKRYKCGCGDGCCTPDLTRKRFKEDGCTTSKWMHIOSKCWN 356

QY 359 CPHANAAFPYFLNDJHKFQ 381  
DB 357 CPHNAAFPYFLNDJHKFQ 379

Search completed: July 8, 2003, 12:28:53  
Job time : 72 secs

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Query Match Similarity	45.0%	Score	951.1	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	LALVYLTILHTRAL- <b>-STCPACRCPPE-APRCA</b> GNGVLA 9 RGCOCGCKVAKALNEDOSK 66	Db		Qy			
11	VAFVFLMLCSRECRGAGCNGCSP- <b>PRPPDPAR</b> PRPPAGVSL 11 DODGCCCGCVAQSLC 70	Db		Qy			
67	TOPCQHKGKLEENRASSTAKGKICRORSGRCPECSNRTI 67 TONGSSTOPPKCKHQCCTDC 126	Db		Qy			
127	AKVCPCLPQZELSLNLUCPNPULPKVYGCCBENCODESTIKDPMQDGLIGEFLD 186	Db		Qy			
130	AVCAGLCCSDNADLSPCOPPKVPPKLGCCBENCODE- <b>-KQD</b> ----- 172	Db		Qy			
187	ASFEVILTRNNEELATAGKQSSKLRL- <b>-PVFGMPBPLKINPLGOKV</b> YQVTTWSQCKTGR 245	Db		Qy			
173	-----T- <b>-TVGVPALAKTFLD</b> EDGPFMI- <b>-T</b> -FRANCVQTEMSSCKTG 215	Db		Qy			
246	GISTYRNNDPECVPRKTCRPEPCCQVPSISKQKCSKTKSPFVNFTACLS 305	Db		Qy			
216	GISTYRNNDASCERKOSLCKVPRPEADELNKKGKCTPK-SKJYJEGSTS 275	Db		Qy			
306	VEKRYPRCPGSDVRECPCTPQLRVYMRRCEDDFESFANMMQSCSKNCHAMER 365	Db		Qy			
276	MKTYRAKFGCVCPTDRCCTPHTTLP-VERKFDSEWYKIMME-IKTCAGTICFGDN 335	Db		Qy			
366	APPFY- <b>-RBLNDI</b> 376	Db		Qy			
336	FESIYVRYMGM 348	Db		Qy			
RESULT 5							
Query Match Similarity	45.0%	Score	950.7	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	YKQVTTWSQCKTGR 245	Db		Qy			
173	RONCONE 5; 273-273; 194 of the human nov proto-oncogene and expression in 1	Db		Qy			
246	AT:Title: Structural analysis of the human nov proto-oncogene and expression in 1	Db		Qy			
216	AT:Reference number: 136065; MUND:943222; PMID:1750150	Db		Qy			
306	AT:Title: Provisional rearrangements and overexpression of a new cellular gene (nov) in myel	Db		Qy			
276	AT:Title: Provisional rearrangements and overexpression of a new cellular gene (nov) in myel	Db		Qy			
366	AT:Title: Provisional rearrangements and overexpression of a new cellular gene (nov) in myel	Db		Qy			
336	AT:Title: Provisional rearrangements and overexpression of a new cellular gene (nov) in myel	Db		Qy			
RESULT 6							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	MEY-196 sequence_revision 11-May-1996 #text_change 05-Nov-1999	Db		Qy			
173	C:Accession: 188069	Db		Qy			
246	C:Accession: 188069	Db		Qy			
216	C:Accession: 188069	Db		Qy			
306	C:Accession: 188069	Db		Qy			
276	C:Accession: 188069	Db		Qy			
366	C:Accession: 188069	Db		Qy			
336	C:Accession: 188069	Db		Qy			
RESULT 7							
Query Match Similarity	45.0%	Score	950.7	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 8							
Query Match Similarity	45.0%	Score	950.7	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 9							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 10							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 11							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 12							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 13							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 14							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 15							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
306	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
276	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
366	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
336	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
RESULT 16							
Query Match Similarity	45.0%	Score	950.6	DB	2;	Length	349;
Best Local Similarity	46.4%	Pred.	No. 1-3e-62;				
Matches	175;	Conservative	57;	Mismatches	101;	Indels	40;
						Gaps	8;
9	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
173	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
246	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db		Qy			
216	EWASCKGKCFPRTYRNRQNCQEMKVKTRICMCRENEEPD-KKCKC-IKTKR 266	Db</					



RESULT 10

MEG6 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Accession: 20-Sep-1999 #sequence\_change 20-Sep-1999 #text\_change 21-Jul-2000

C:Accession: T19394

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

GenBank

M1: Identification of high-molecular weight proteins with multiple EGF-like motifs

M1: Reference number: 214246; MVID:8560089; PMID:969303

M1: Status: preliminary

M1: Molecule type: mRNA

M1: Residues: 1-1574 <WAK>

M1: Cross-references: EMBL:AB011322, NID:93449293; PIDN:BAH3462.1; PID:93449294

M1: Experimental source: strain Sprague-Dawley; brain

M1: GenBank

M1: GeneID: MEG6

Query Match 7.48; Score 156; DB 2; length 1574;

Best Local Similarity 7.2%; Score 153; DB 2; length 837;

Matches 97;保守性 37%; Mismatches 132; Indels 176; Gaps 28;

Query 26 CPACAGCPC-----LBPKAPAEV-----GLVRDGG----- 50

Db 568 CSEPTCCTONGCDPDPVIGACRCPGSGAICGEGPKPCKGKCKRKHANINGRGRHLY 627

Db 51 GCKCKVAKQK-----NEDCSKTPQDPKELCNGASSTALKGKCR 92

Db 628 GAC-LCDGPGYGFSGHACAPWAEPGSGEDCICQ-SBTRSCPKDGS-----CK 678

Db 93 AOSBEGPCEPTNRTQNGESFOPKHOCTGIDAVGCGI-----CPO 136

Db 679 AEGPQERGQAC-EES-PFGGGERHRCG-VADQDVSE-RTCPGPGQDQG 73

Db 137 EUSLNLG-----QPNPLVYKVTGQC-CBEWCGDSDS1KUPMDGGLKELEGDA 187

Db 734 ECPVTPVWCGSGCGSCVCGPCHYRGTGCG-CPGKGDGACCGPBGNSQEL----- 789

Db 188 SEVETTRNNELIATVKGSSKLRUPVFGNPERILYMPLOGKCTWTSWSKSKT----- 243

Db 790 -----CPACBHGSC-----APPTGCGLCLDFPGSGCQDTGAGW 825

Db 244 -GTG-GSTR-VTNDNAPQRWKTPKTRICEVPRCPQPVYSSKKRKCSRTKSKSPVPRY 300

Db 826 YGFGGTCRACGAC-HDPPGPGC-----APWPGGSCORACGSGHGD----- 872

Db 301 ACGLSVKVKYRPGC-----GSC-----VDRG-----CT-----POLTRVWRP-----RCBDGTTFSR 345

Db 873 -C1-----IUPNCAGHIGNDAVGGLCAGEYEGPFCDSOCDROGYVPSCE----- 918

Db 346 IYPMAMOSKONTN-CPEHANE 365

Db 919 -----OKCROHACDHWGSA 935

RESULT 12

Thrombospondin Precursor - chicken

C:Species: Gallus gallus (chicken)

C:Accession: 10-Sep-1999 #sequence\_change 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A39804

R:Lawler, J.; Duquette, M.; Ferro, P.

J: Biol. Chem. 266, 8039-8043, 1991

A:Title: Cloning and sequencing of chicken thrombospondin.

A:Reference number: 214246; MVID:91217026; PMID:2022631

A:Status: preliminary

A:Molecule type: mRNA

A:Cross-references: GB:MG6055; NID:9212763; PIDN:AA51437.1; PID:9212764

C:Superfamily: thrombospondin 1; BGP homology: thrombospondin type 1 repeat homology <WAK>

F:35-389/Domain: von Willebrand factor type C repeat homology: thrombospondin type 1 repeat homology <WAK>

F:442-498/Domain: thrombospondin type 1 repeat homology <WAK>

RESULT 11

A42112 mucin-like peptide MLP 2677 - rat



Search completed: July 8, 2003, 12:31:40  
Job time : 43 secs

סבבון כהן : allIT 200 802

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Gencore version 5.1.6

Run on: JULY 8, 2003, 12:13:12 ; Search time 23 Seconds

without alignments) updates/sec

687.004 Million cell

Title: US-09-901-910-2

Prefect score: 2115

Sequence: 1 MSRRFARALAVVTLHTR.....ANEARPPYRFLNDIHKFRD 381.

Scoring table: BIOSUM62

6Pep 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-Processing: Minimum Match % 0%

Maximum Match 100%

Listing first 45 summaries

Result NO. Score Query Match Length DB ID Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

SwissProt\_40.0

FBILL-HUMAN

P23142 homo sapien

### ALIGNMENTS

RESUME

CYR61-HUMAN

P09888 homo sapien

P0

















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DR	EMBL: US7063; AMB1706; 1; -;	ID NO_MOUSE
DR	InterPro: IPR000359; Cys_knot; -;	AC STANDARD: PRT: 354 AA.
DR	InterPro: IPR000867; insl_gro_fac_pr; -;	DT 06/29/97; Rel. 35 (Created)
DR	InterPro: IPR000884; TSP1; -;	DT 01-NOV-1997 (Last sequence update)
DR	InterPro: IPR001007; WME_C; -;	DT 15-JUN-2002 (Rel. 41, last annotation update)
DR	InterPro: IPR001007; WME_C; -;	DT 15-JUN-2002 (Rel. 41, last annotation update)
DR	PFam: PF00090; tsp_1; 1; -;	DE Nov protein homolog precursor (NOVH) (Nephroblastoma overexpressed gene protein),
DR	PFam: PF00093; wmc_1; 1; -;	DE GN NOV,
DR	PFam: PF00219; IGFBP_1; 1; -;	OS Mus musculus (Mouse)
DR	SMART: SM00011; CT_1; 1; -;	OC Bivalvia: Mollusca; Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus: MCB1_TAXID=10990;
DR	SMART: SM00011; IB_1; 1; -;	OX RN
DR	SMART: SM00229; TSP1; 1; -;	RP STRAIN=129/SV and ICR: TISSUE=Brain;
DR	SMART: SM00229; WMC_1; 1; -;	RX MEDLINE-97130523; Pubmed=6957571;
DR	SMART: SM00229; WMC_1; 1; -;	RA Smith R, R, Narasimhan D, Taylor L B, Choi C P, Martinierie C, Perbal B, Schonied P N, Boulet C A;
DR	SMART: SM00229; WMC_1; 1; -;	RT "Genomic structure and chromosomal mapping of the mouse nov gene.", Rl Genomics 38:425-429 (1996).
DR	PROSITE: PS01222; WMC_BINDING; 1; -;	RN 22
DR	PROSITE: PS01208; WMC_1; 1; -;	RP SEQUENCE FROM N_A.
DR	PROSITE: PS01185; CTRK_1; FALSE_NEG; -;	RC STRAIN=5710/6;
DR	PROSITE: PS01225; CTRK_2; 1; -;	RX MEDLINE-9620003; Pubmed=6622864;
DR	KW growth factor binding; Signal; -;	RA Martinierie C, Chevalier F, J, Rauscher F, J, III, Perbal B, ;
FT	SIGNAL 1 18; -;	RT "Regulation of nov by Wnt: a potential role for nov in neurogenesis.",
FT	CHAIN 1 9; 343; -;	RT Oncogene 12:147-149 (1993).
FT	DOMAIN 1 93; 159; -;	CC 1 FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION (BY SIMILARITY).
FT	DOMAIN 1 249; 323; -;	CC -1 SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY CTRF-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.
FT	DISULFID 1 249; 286; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
FT	DISULFID 1 266; 300; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
FT	DISULFID 1 277; 316; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
FT	DISULFID 1 280; 318; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
FT	DISULFID 1 285; 322; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
FT	CARBOHYD 1 265; 265; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
FT	SEQUENCE 343 AA; 38700 MW; 677D708B21316F CTR64; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
FT	QUERY Match 39/28; Score 829.5; Pred. No. 8 5e-55; Length 343; Best Local Similarity 42.18; Pred. No. 8 5e-55; Matches 159; Conservative 43; Mismatches 113; Indels 63; Gaps 9; -;	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
QY	9 LALVYVLLHMLTALSTCRAA--KCPPEAKPAAKPGVYDGGCGVCAKQINDESKT 67	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
Db	5 LALCFIL--IIVVSKCPSDODCPPEPPSAPSVLINDGCGCVCAGCGESESHL 63	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
QY	68 OPRCNGKLGICFCAASAKALKICABSERKCEVNRISITVYDGFSPNPKHCTCING 127	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
Db	64 NPCDGDGLYCENFADNRPRYCTCA-LEGSNCVDPYDVRBVRFSPSKYHCING 122	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
QY	128 YCQCPCLCPDSEPLNCGCNPLVYKVGOCCEAWCUDPESDSTKDPDQDLS 180	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
Db	123 TGCYCPNCLDULLPGCPCEPPRKYVGOCCKWCSK---KEMK---ATGGFAMAM 174	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
QY	181 --YEGEGDASVELTNNIHLIAVKGSSKSLKQVPEMPRTVYQIPLQKIVTWS 237	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
Db	175 RPEATLIDASPSFA-----CIAQTEPE 199	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
QY	238 QCCSKCTCCTISPRVNIDNPCLVKEPRTECEVPC--GQPVYSSKTKRKKRKSSTKSP 296	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
Db	200 ACSKTCCOMVSSRVRNBRACRQKQLMRCSSESEPRWVKEKSKKVKRVRKTP 259	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
QY	297 RPTAGCQLSLKVKYKQGSCSDVCGTQDTRKARRFDDGEGTSKNNMDSKCN 356	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
Db	260 HEHKHCNTSQTQYKTCRCCOCDSCTPHTSKTMVHEWFCFKRKKVPPVAVSTVCH 319	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
QY	357 YNCP-----HANAEAP 368	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
Db	320 YNCPQDQSLQVWENAEF 337	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.
RESULT 12	NO_MOUSE	CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTRK) DOMAIN.





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QY 262 :KEKTCVEWRC----->QPYPLSLAKG 283
Db 487 :RETECKEAKCPNGOMKPSWPSACTWGGGIRHESRLCHNSPPOVgkrcvdpukh 546
QY 284 :KCKSTKTSPEPRTYAGLSVSKYRPPKCCSCVDPG->CSCP 325
Db 547 :DNCNK-RUCP----->DGCLSNPDPQARCNNSYFPGSRSACGP 582

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Search completed: July 8, 2003, 12:29:23  
Job time : 25 secs

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InterPro: IPR00884 TSP1.
InterPro: IPR01128 TSPN.
InterPro: IPR01071 TSP-C.
InterPro: IPR03367 TSP-3.
PFam: PF00090: EGF_1_3.
PFam: PF00093: FWC_1.
PFam: PF02210: TSPN_1.
PFam: PF02412: TSP-3_8.
SMART: SM00011: EGF_2_2.
SMART: SM00001: EGF_1_1.
SMART: SM00209: TSP1_3.
SMART: SM00244: VWC_1.
PROSITE: PRO00024: EGF_1_1. FALSE_NEG.
PROSITE: PRO01186: EGF_2_1_1.
PROSITE: PRO00092: TSP1_3.
PROSITE: PRO01208: FWC_1.
PROSITE: PRO01208: FWC_1.
Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
EGF-like domain; Signal

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Qy	237	SOCSSKGIGISRTWNDNPDRKVKETRICVDRGCPGPPYSSIKKGKCSKTKKSPPV	296	Oy	323	CPOLPDTYMRFRGEGECPNSNAMTQSCCKNCHANE-RAFPYRFLNDI	376
Db	206	SACSTGIGISTRNDNPFLRKLKSRMCRWCRBDELINGKKGKJLKPRAKPV	265	Db	287	CPRHTRALIEVERKCPDSEVMKNNMKTACFHNCGONDIFERMYRMGDN	342
Qy	297	RTPYAGGSLSKYKRYKCGCSDGCTPRTTIPKMFRCGEGTSFKNMQLSCCN	356	Oy	296	KRFSGTSKTYKRYKCGCSDGCTPRTTIPKMFRCGEGTSFKNMQLSCCN	325
Db	266	KRFSGTSKTYKRYKCGCSDGCTPRTTIPKMFRCGEGTSFKNMQLSCCN	325	Db	357	YCPHANBAFPY-SLFDI	376
Qy	357	YCPHANBAFPY-SLFDI	376	Oy	357	YCPHANBAFPY-SLFDI	376
Db	326	YCPHDFNDTIFESLTYRMKD 347		Db	173	YCPHDFNDTIFESLTYRMKD 347	
RESULT 8							
Qy	094607	PRELIMINARY;	PRT;	Qy	094607	PRELIMINARY;	PRT;
Ac	04607;			Ac	04607;		
Db	01-JAN-1998	(REMBUREL. 05, Created)		Db	01-JAN-1998	(REMBUREL. 05, Last sequence update)	
Db	01-JUN-2002	(REMBUREL. 21, Last annotation update)		Db	01-JUN-2002	(REMBUREL. 21, Last annotation update)	
Db	01-JUN-2002	(REMBUREL. 21, Last annotation update)		Db	01-JUN-2002	(REMBUREL. 21, Last annotation update)	
Db	01-JUN-2002	(REMBUREL. 21, Last annotation update)		Db	01-JUN-2002	(REMBUREL. 21, Last annotation update)	
Os	Xanthopus laetus (African clawed frog)			Os	Xanthopus laetus (African clawed frog)		
Os	Amblyota; Metacoda; Chordata; Vertebrata; Euteleostomi;			Os	Eukaryota; Metacoda; Chordata; Craniata; Vertebrata; Euteleostomi;		
Os	Xanthopodidae; Xenopus.			Os	Archaeozoa; Nves; Neognathae; Galliformes; Phasianidae;		
Os	NCBI_TaxID:8351;			Os	Gallus gallus (chicken)		
RN	1)			RN	1)		
SEQUENCE FROM N.A.							
RA	Ying Z., King M.L.			RA	Ying Z., King M.L.		
RL	Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.			RL	Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: U03524; ABAB659; 1;			DR	EMBL: U03524; ABAB659; 1;		
DR	EMBL: U03533; C8;			DR	EMBL: U03533; C8;		
DR	INTERPRO: IPR00359; Cys_knot.			DR	INTERPRO: IPR00359; Cys_knot.		
DR	INTERPRO: IPR00867; Insl1_gro_fac_pr.			DR	INTERPRO: IPR00867; Insl1_gro_fac_pr.		
DR	INTERPRO: IPR00884; TSP1.			DR	INTERPRO: IPR00884; TSP1.		
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Db	306	VVKTPYKCGVDRGRCRCPOLTRVNMVKPRCDEGEFTEKSNMMQSCKNCNPHANER	365
Db	271	VTVTRFKCOPRQGRCRCPOLTRVNMVKPRCDEGEFTEKSNMMQSCKNCNPHANER	330
Qy	366	AEPPY - RLFDI	376
Qy	331	FESLYKRYGMID	343
Db	169	- EOTRVGPALAVYQDGTGDSMTR	209
RESULT 10			
OPR#0			
ID	OPR#0	PRELIMINARY;	PRT: 347 AA.
AC	OPR#0;		
DT	01-MAY-2000	(TREMBLREL. 13, Created)	
DT	01-MAY-2000	(TREMBLREL. 13, Last sequence update)	
DT	01-JUN-2002	(TREMBLREL. 21, Last annotation update)	
DE		Connective tissue growth factor	
GN		CTGF	
OS		Nototophthalmus virideceps (Eastern newt) ( <i>triturus virideceps</i> )	
OC		Budivaria; Metacosa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC		Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;	
OC		Notophthalmus;	
OX		NCBI-TaxID:8316;	
RN		11)	
RC		SEQUENCE FROM N.A.	
RA		TISSUE=FORELIMB BLASTEMA;	
RA		Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.	
RL		[12]	
RP		SEQUENCE FROM N.A.	
RC		TISSUE=FORELIMB BLASTEMA;	
RA		MEDLINE=9903008; PUBMED=9813273;	
RA		Cach D.E., Gates P. B., Imokawa Y., Brookes J.P.:	
RT		Identification of newt connective tissue growth factor as a target of retinoid regulation in limb blastemal cells.;	
RL		Gene 22:119-124(1996).	
EMBL		CB47161; CAB6995; 1;	
DR		Interpro: IPR00339; Cys.knot;	
DR		Interpro: IPR00867; insl-gro_fac-pr.	
DR		Interpro: IPR00884; TSP1.	
DR		Interpro: IPR00107; VWF_C.	
DR		Pfam: PF00019; IGFBP_1.	
DR		Pfam: PF00090; TSP1_1.	
DR		Pfam: PF00093; VWF_C.	
DR		SMART: SM00041; CT_1.	
DR		SMART: SM00121; IB_1.	
DR		SMART: SM00209; TSP1.	
DR		SMART: SM00224; VWF_C.	
DR		PROSITE: PS01183; CTOK_1.	
DR		PROSITE: PS01226; CTOK_2.	
DR		PROSITE: PS02226; IGF_BINDING.	
DR		PROSITE: PS02208; VWF_C; UNKNOWN.	
SEQUENCE	347 AA;	38098 MW;	387E2399F27672C1 CRC64;
Query Match	45.3%	Score 920.5;	DB 13;
Best Local Similarity	45.4%	Pred. No. 2,76-80;	Length 347;
Matches	171;	Conservative	48; Mismatches
		107;	Indels 51; Gaps 6;
Qy	9	LALVUTLHLTRALSTPQCRACNHCOPVQGIVLUDCGCGCKVCKNLDKSKQ	68
Db	12	LQALVAVLWVCA-QCSCGEQCRPKPPCPGACTSPLVSDCGCGCKVCKNLDCTERD	70
Qy	69	PDQITKOLCNGGASSTALKGCKQASDPERPENERTIQNGESFOPNQKICDGAV	128
Db	71	VDPHPRGUCDGSVRVKKIGVCFK-DCACRUGENAVRSGESFOPNQKICDGAV	129
Qy	129	GQICPQDQSLPQGCPGPRVWVQGCPQEWQDSDKPKPQDQGILGKELFDAS	188
Db	130	GGCPVQCVWRPLSPQCPGPVWVQGCPQEWQDSDKPKPQDQGILGKELFDAS	169
Qy	189	EVETRNLINLAV-----GKSKLKRUPFGMPEPRIMLPLQGOKCIVOTWSQCS	241
Db	170	-----KOHIVVGPALAYLSDGDPHMM-----RANCIVWPTTCAKCKG	216
RESULT 11			
ID	097765	PRELIMINARY;	PRT: 349 AA.
AC	097765;		
DT	01-MAY-1999	(TREMBLREL. 10, Created)	
DT	01-MAY-1999	(TREMBLREL. 10, Last sequence update)	
DT	01-JUN-2002	(TREMBLREL. 21, Last annotation update)	
DE		Connective tissue growth factor.	
GN		CTGF	
OS		Sus scrofa (Pig).	
OC		Budivaria; Metacosa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC		Mammalia; Batrachia; Cetartiodactyla; Suina; Suidae; Sus.	
NCBI-TaxID:9823;		[11]	
RP		SEQUENCE FROM N.A.	
RC		TISSUE=VERUS;	
RA		Cloning and sequencing of a porcine connective tissue growth factor (CTGF) cDNA.	
RT		Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.	
RL		[12]	
DR		EMBL: U70000; ADDON141; 1;	
DR		Interpro: IPR00359; Cys.knot;	
DR		Interpro: IPR00867; insl-gro_fac-pr.	
DR		Interpro: IPR00884; TSP1.	
DR		Interpro: IPR00107; VWF_C.	
DR		Pfam: PF00019; IGFBP_1.	
DR		Pfam: PF00090; TSP1.	
DR		Pfam: PF00093; VWF_C.	
DR		SMART: SM00041; CT_1.	
DR		SMART: SM00121; IB_1.	
DR		SMART: SM00209; TSP1.	
DR		SMART: SM00224; VWF_C.	
DR		PROSITE: PS01183; CTOK_1.	
DR		PROSITE: PS01226; CTOK_2.	
DR		PROSITE: PS02226; IGF_BINDING.	
DR		PROSITE: PS02208; VWF_C.	
SEQUENCE	349 AA;	37946 MW;	35AB4275AC1D4B3A CRC64;
Query Match	41.7%	Score 882;	DB 6;
Best Local Similarity	43.5%	Pred. No. 1,36-80;	Length 349;
Matches	162;	Conservative	59; Mismatches
		111;	Indels 40; Gaps 7;
Qy	10	ALVUTLHLTRAL-STPQCRACNHCOPVQGIVLUDCGCGCKVCKNLDKSKQ	67
Db	12	AVVLLALSPRASQGCGQACKRACPGAVSLLGCGCGCKVCKNLDCTERD	71
Qy	68	QCPHTRGECFASSTALKGCKQASDPERPENERTIQNGESFOPNQKICDGAV	127
Db	72	ACCPHPRGUCDGSVRVKKIGVCFK-DCACRUGENAVRSGESFOPNQKICDGAV	130
Qy	128	VCCTPQDQSLPQGCPGPRVWVQGCPQEWQDSDKPKPQDQGILGKELFDAS	187
Db	131	VCPICLSPVMDLSPCPDPGCPVWVQGCPQEWQDSDKPKPQDQGILGKELFDAS	169
Qy	188	SEVELTNNELVAKGKSKLKRUPFGMPEPRIMLPLQGOKCIVOTWSQCS	246





DR	DR	DR
PROSITE, PS01225; PROSITE, PS01185; CTRK2; 1.	PROSITE, PS01208; UNKOWNL1.	PROSITE, PS01208; UNKOWNL1.
SEQUENCE 367 AA: 40513 MW: 84434C69D3243D2 CRC64;		
Query Match	Best Local Similarity	Length
Matches 149; Conservative 38%; Minatches 52; Indels 55; Gaps 8;	35.9%; Score 759; DB 11;	367;
QY	5 TALARALVYLHHLTRIALST-----CPAAGCPIEAPKACPAVATVADGCCWVKA 57	
Db	21 LALALSTSPPTPTPAPLEENTRPFPCKWCEPAPPPRLGYSIMDCCCKCA 80	
OY	58 KOLBACBCKTSPCTGKLCLECP-GASSPAKGTCRASSGSPAPBMSRIVNGESEPH 116	
Db	81 QQLDQKTRTAAVCPHGLYCDYSSDPRTVAGIC-AQWVGEVIGVAYNGSQQP 139	
OY	117 CKHOCCTGAGGATGTC-POEELSLNPGCPNPLKTYGOCCEWENPDESIDPMPD 174	
Db	140 CRYNCCTGCTGTCPTCPLSPRP-----PRLMCQPHKRYWGCCECNCDQDRR-- PR 193	
OY	175 QDGLIGEKGFASEVELTRNELLANGKSSKLKRLPVTGOMEPRLINPQGKCIWTT 234	
Db	194 QALDTRRAFAASGAAVQKRYEN-----CIAINTS 221	
OY	235 SRSQSCCTGCGTQGTCSTRTRNNDPCCRLLKKEPCEVPGCOPGTYVSSLLKKGKSKKSKKSSP 294	
Db	224 PHSCTGCGTQGTCSTRTRNNDPCCRLLKKEPCEVPGCOPGTYVSSLLKKGKSKKSKKSSP 281	
OY	295 PFRRTYGGCQLSKKTRKCGCSDYGCCTPQLRTVKGKRPKCEGEGTFSKPKMMGSK 354	
Db	282 ATNTFLDAGCUSTKTRKCGCSDYGCCTPQLRTVKGKRPKCEGEGTFSKPKMMGSK 341	
OY	355 CWCYCPHAAEAAFFYVLFNDHFRD 381	
Db	342 CWCSCRNPD-----IFADLSEPP 361	

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